

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,061

1643

DATE: 09/16/98
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This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Huse, William D.
6 Glaser, Scott M.
7
8 (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
9 Antibodies, Nucleic Acids Encoding Same and Methods of Use
10
11 (iii) NUMBER OF SEQUENCES: 100
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Campbell & Flores LLP
15 (B) STREET: 4370 La Jolla Village Drive, Suite 700
16 (C) CITY: San Diego
17 (D) STATE: California
18 (E) COUNTRY: United States
19 (F) ZIP: 92122
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 09/016,061
29 (B) FILING DATE: 30-JAN-1998
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US 08/791,391
34 (B) FILING DATE: 30-JAN-1997
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Campbell, Cathryn A.
38 (B) REGISTRATION NUMBER: 31,815
39 (C) REFERENCE/DOCKET NUMBER: P-IX 2965
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (619) 535-9001
43 (B) TELEFAX: (619) 535-8949
44
45
46 (2) INFORMATION FOR SEQ ID NO:1:

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 351 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: both
52          (D) TOPOLOGY: linear
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 1..351
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG      48
63      Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
64          1              5              10              15
65
66      TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT      96
67      Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
68          20              25              30
69
70      GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC      144
71      Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
72          35              40              45
73
74      GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG      192
75      Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
76          50              55              60
77
78      CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC      240
79      Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
80          65              70              75              80
81
82      CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT      288
83      Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
84          85              90              95
85
86      GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA      336
87      Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
88          100              105              110
89
90      GTG ACT GTT TCT AGT      351
91      Val Thr Val Ser Ser
92          115
93
94
95      (2) INFORMATION FOR SEQ ID NO:2:
96
97          (i) SEQUENCE CHARACTERISTICS:
98              (A) LENGTH: 117 amino acids
99              (B) TYPE: amino acid

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100 (D) TOPOLOGY: linear

101

102 (ii) MOLECULE TYPE: protein

103

104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

105

106 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
107 1 5 10 15

108

109 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
110 20 25 30

111

112 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
113 35 40 45

114

115 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
116 50 55 60

117

118 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
119 65 70 75 80

120

121 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
122 85 90 95

123

124 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
125 100 105 110

126

127 Val Thr Val Ser Ser
128 115

129

130 (2) INFORMATION FOR SEQ ID NO:3:

131

132 (i) SEQUENCE CHARACTERISTICS:

133 (A) LENGTH: 321 base pairs

134 (B) TYPE: nucleic acid

135 (C) STRANDEDNESS: both

136 (D) TOPOLOGY: linear

137

138

139 (ix) FEATURE:

140 (A) NAME/KEY: CDS

141 (B) LOCATION: 1..321

142

143

144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

145

146 GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA 48
147 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
148 1 5 10 15

149

150 GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC 96
151 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
152 20 25 30

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153
154   CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC      144
155   Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
156           35                      40                      45
157
158   AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC      192
159   Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
160           50                      55                      60
161
162   AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT      240
163   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
164           65                      70                      75                      80
165
166   GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
167   Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
168           85                      90                      95
169
170   ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG      321
171   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
172           100                      105
173
174
175   (2) INFORMATION FOR SEQ ID NO:4:
176
177       (i) SEQUENCE CHARACTERISTICS:
178           (A) LENGTH: 107 amino acids
179           (B) TYPE: amino acid
180           (D) TOPOLOGY: linear
181
182       (ii) MOLECULE TYPE: protein
183
184       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
185
186   Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
187       1           5           10           15
188
189   Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
190           20           25           30
191
192   Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
193           35           40           45
194
195   Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
196           50           55           60
197
198   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
199           65           70           75           80
200
201   Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
202           85           90           95
203
204   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
205           100          105

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207 (2) INFORMATION FOR SEQ ID NO:5:

208

209 (i) SEQUENCE CHARACTERISTICS:

210 (A) LENGTH: 351 base pairs

211 (B) TYPE: nucleic acid

212 (C) STRANDEDNESS: both

213 (D) TOPOLOGY: linear

214

215

216 (ix) FEATURE:

217 (A) NAME/KEY: CDS

218 (B) LOCATION: 1..351

219

220

221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

222

223 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG 48

224 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg

225 1 5 10 15

226

227 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT 96

228 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr

229 20 25 30

230

231 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC 144

232 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val

233 35 40 45

234

235 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG 192

236 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val

237 50 55 60

238

239 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC 240

240 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr

241 65 70 75 80

242

243 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT 288

244 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys

245 85 90 95

246

247 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG 336

248 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu

249 100 105 110

250

251 GTC ACT GTC TCT GCA 351

252 Val Thr Val Ser Ala

253 115

254

255

256 (2) INFORMATION FOR SEQ ID NO:6:

257

258 (i) SEQUENCE CHARACTERISTICS:

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SEQUENCE VERIFICATION REPORT
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